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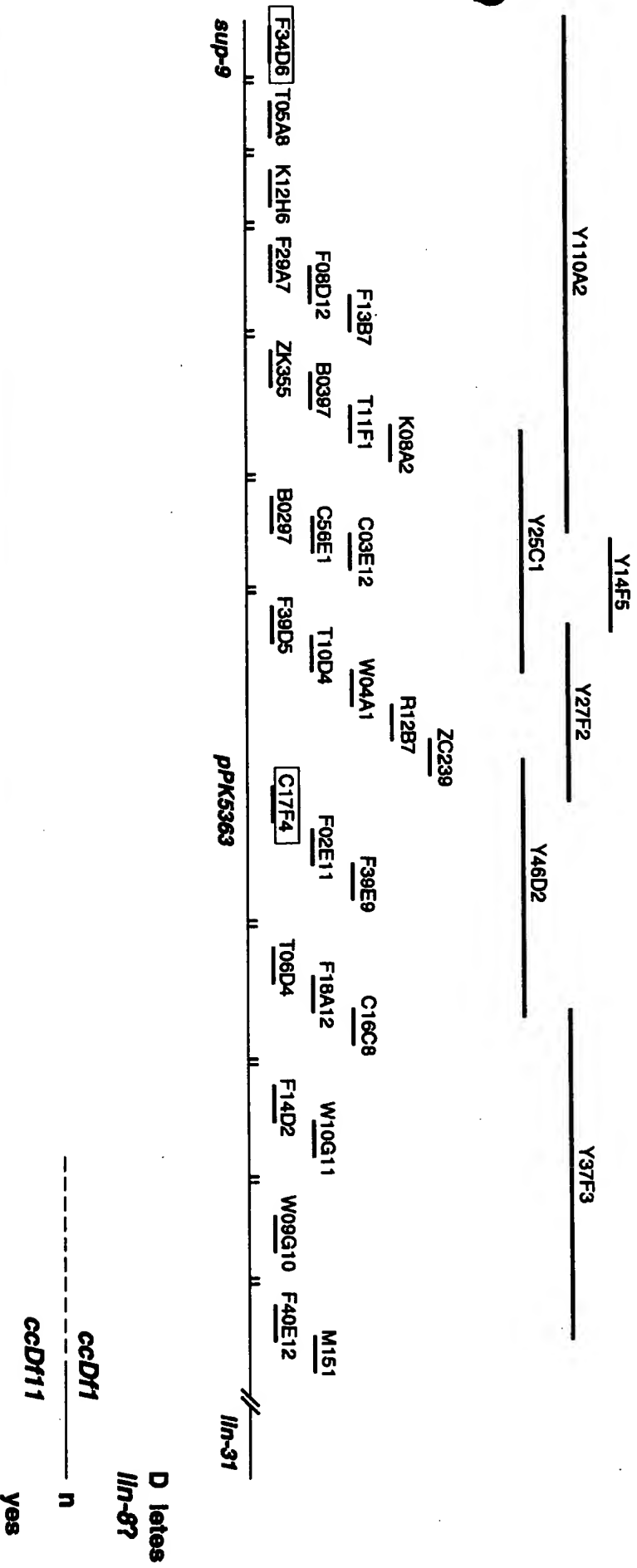
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FIG. 1



*iln-8*

D letes  
*iln-8?*

*ccdH1*

n

*ccdH11*

yes

FIG. 2

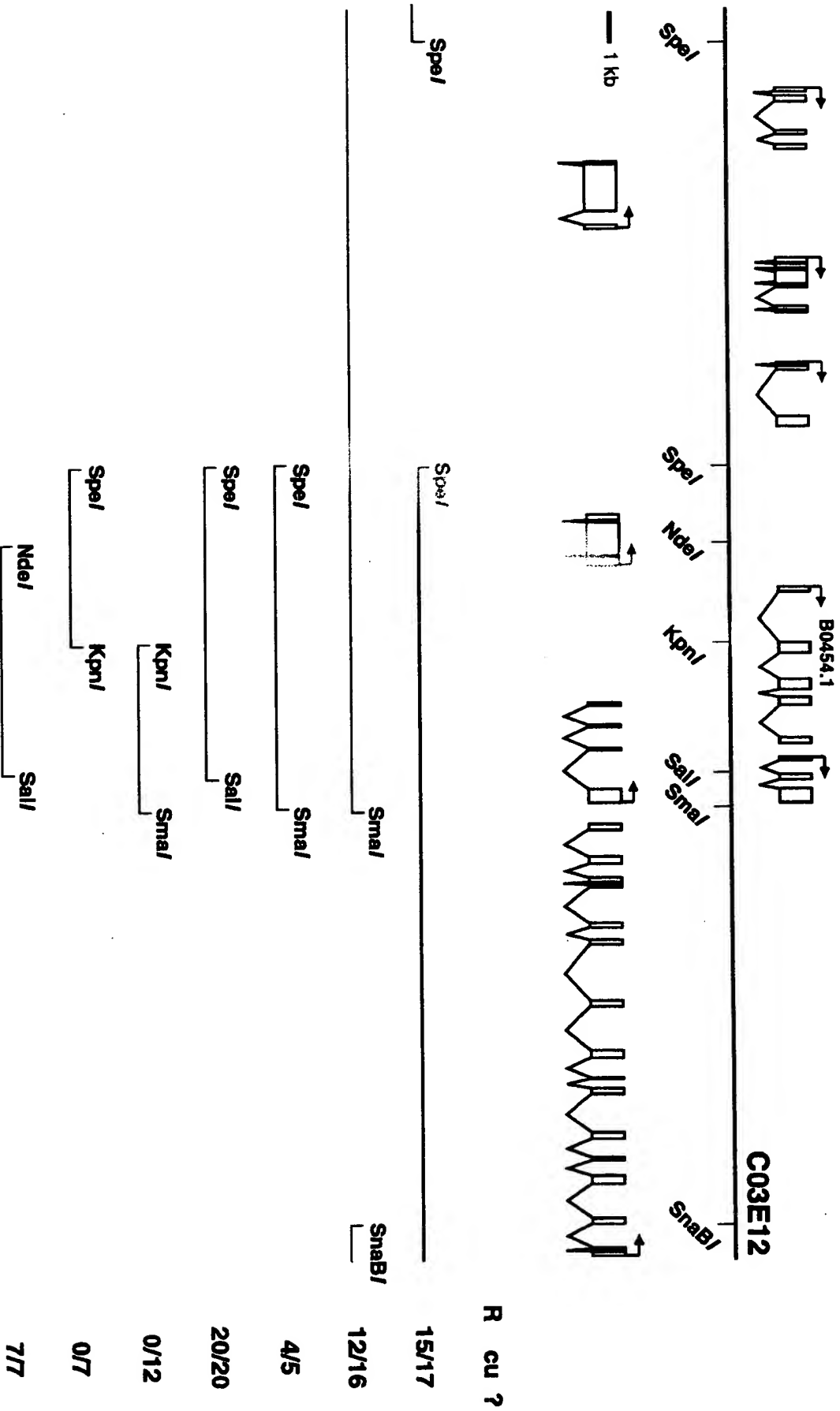


FIG. 3

LN-8 K THSTGSKRTVPFYKL VPLP PDP RYFSTK IALSKD FK DDYDVN ETL NEIGKC 75  
C41H7.3 LS QE-----LLDAP PAAT I--HRISLSG RNI--HAKS LKTM LCVRR SLEENR 62  
C41H7.4 L QE-----HMH RAIT A--HQITL EKER-- KDYVRDATK ASV SLKDH 60  
C41H7.5 L QE-----HMN RTIT P--HQITL EKER-- V RDYVRNATK TSL SLIKDR 60  
C41H7.6 LN QE-----GVADA RALT I F--IHVSM E MGM-- LNSVYEATK SAL DLKDR 61  
C08A9.6 MNP EE--PRFSIVPLPR RPTT I--SHCITMAD LLL-- NTK HKTATRAPKI L SLKDR 67  
C08A9.7 VSATRV--PRRSTTSATAQRTPS M A--SFPTMDE LEK-- NRE VVNASK IAM LA TLELY 68  
F14D2.2 R QE-----QVNPP RAIT A--HRITMDE KKR-- KDYVRDATK ASV SLKDY 62

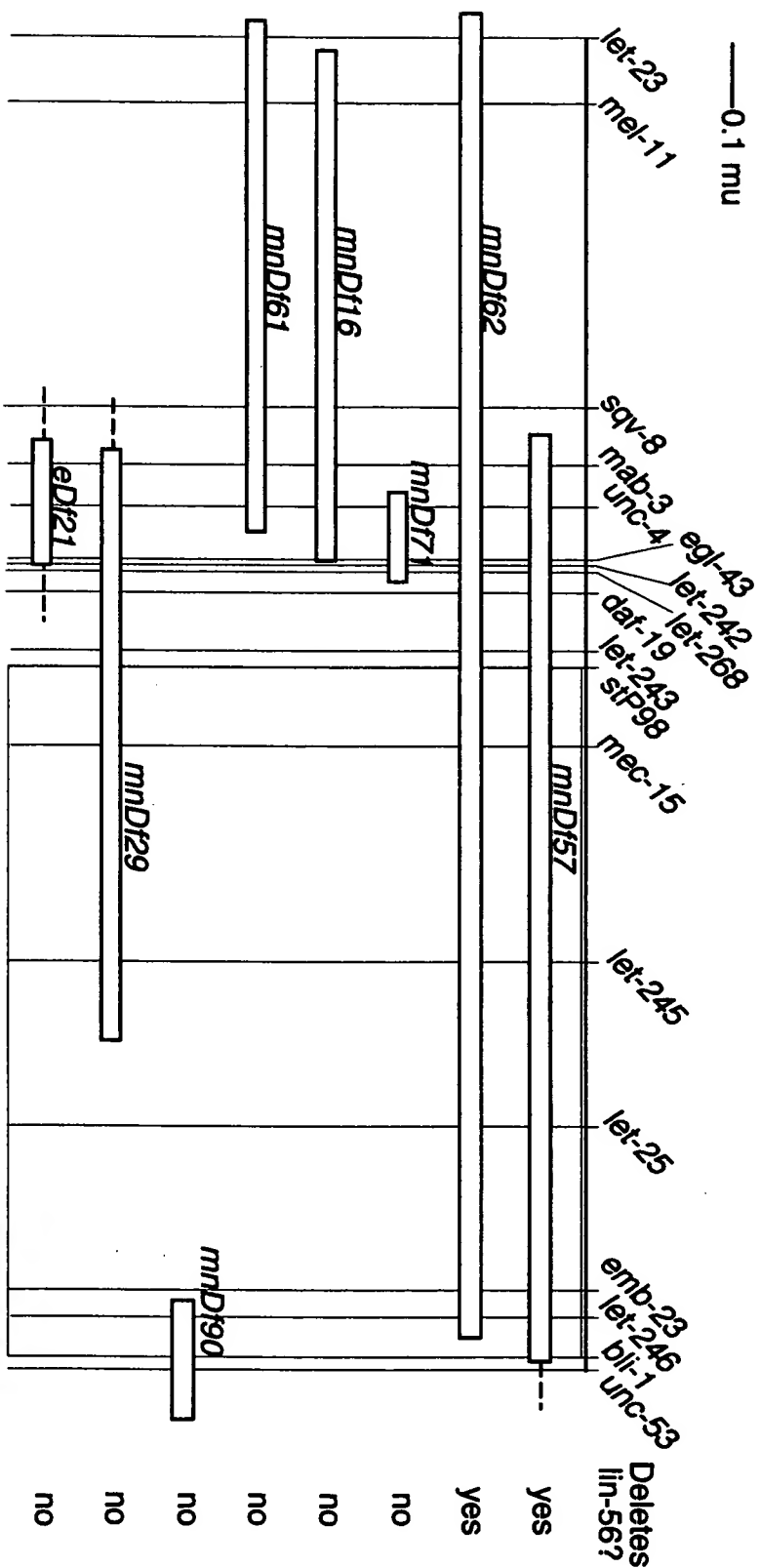
LN-8 DI SSRSQAIMEHYPIVAT TR LLL-----IKS KQIYKC DN RNR RVA VS R TP QV Y 143  
C41H7.3 RAL IRVHKSPKADWEVLGV VFE KAV-----VKQ QRIFLTARDW RRN QLY IQRKMDKLTLD E 129  
C41H7.4 GM QNGNRFOPEKWRALGV-DV Q QIV-----RVNDRMKMLVM SV KKKIAIC RD K DR AT KD 127  
C41H7.5 KAM APAKPSEDKWQLGA-VFS KVV-----VTQ RRLVSS HV KTKMSHC KV KMDRVST Y 134  
C41H7.6 GM QNGNRFOLENWRELGV-DV Q QIVRAELGEV VNDMHRMFVV AV KQKITVC RY K DR AT D 128  
C08A9.6 EI DRKAQFSAKNWQLGV-V E YIV-----RSND HKMLRTA VV KNK RTC GIK DR AT TE 134  
C08A9.7 EM KPGGPMVAKKWQAFGA-M R KIV-----RCKD HSVFTLT SSIKRK RTC LI RMHRSKTDEE 135  
F14D2.2 DM QNGNRFOQTRKWRALGV-V Q QIV-----GVDDMRKMFMS TV KQKITFC RNMKMDR AT D 129

LN-8 M R F GFIR DYTQRW D LKDLVDVLGLEAR ASKNMEKVDS LMEPMEPM STMDEMCEP P... 214  
C41H7.3 LAK L PHFI QYLGQF H-----GEE-----WT LY-----D DIICDGMQV V... 177  
C41H7.4 L Y Y RHFL ETLGQF N-----GEE-----WT DQIQDE--DIYDGMLDGDL... 178  
C41H7.5 L N F RHFL EMLDRF N-----GKQ-----WT DQPTDD-D DIICDGIFF V M... 186  
C41H7.6 L QN F RHRER ETLGQF N-----GEQ-----WT DQPADD-D DIYDGIFF V M... 180  
C08A9.6 L K Y PHFI ETLGHF N-----GEP-----WD AHIDDD-D DIYEGYV ADK... 186  
C08A9.7 M K Y L PYFQ QSIGQF K-----DEP-----WT DQAQED--DILFDGLF V N... 186  
F14D2.2 L QN Y RHFL QTLGKF K-----GEQ-----WI DQVEDDDE DVIIFDGES 178

LN-8 EEMNQ TY AI IAREQ E L K L K DVV FDDQK--ADV YR QKNS 386  
C41H7.3 ...EDSVSYTKITEDLLOKK HKHRFI Q KTIM LDDDEV TELA FG I EQSNVVRRLRLQROQQRGREGQ 366  
C41H7.4 ...RSAQH AE AK LFLOQ EKSNI I ETM KTI FDDPSAD QNV EIFD AQEA AKKRRAENRAQREQ 331  
C41H7.5 ...STAEQ GEEID LIQLY Q EM I Q F KTI F LEDET V FSNL FE EQENFKRRRSRAQRL 327  
C41H7.6 ...STAEQ GEEID LIQLY Q EM I Q F KTI F LEDET V FSNL FE EQENFKRRRSRAQRL 321  
C08A9.6 ...NSAQH GE VH LFAQY E SK F ET KTI LEEP--EHA AEVFT QSETAKRRRSRSEATWQNGQ 344  
C08A9.7 ...KTADN GD VKQLFVDH D ANFF EV KTV ELRDP--AFTNA VFFDEMSSLES AKRRRSRSEMKN 331

FIG. 4

— 0.1 mu



lin-56

*T01E8*  
*R05H5*  
*F33H1*  
*F27E5*  
*ZK945*  
*C18D1*  
*VM02G9R*  
*M02G9*  
*ZK970*  
*ZK971*  
*F54B3*  
*T09F3*  
*E04D5*  
*ZK673*  
*ZK666*  
*F59B10*  
*R166*  
*C14A4*  
*M28*  
*D2089*  
*C09G5*  
*C06A1*

stP98

— 25 kb

bli-1

FIG. 5

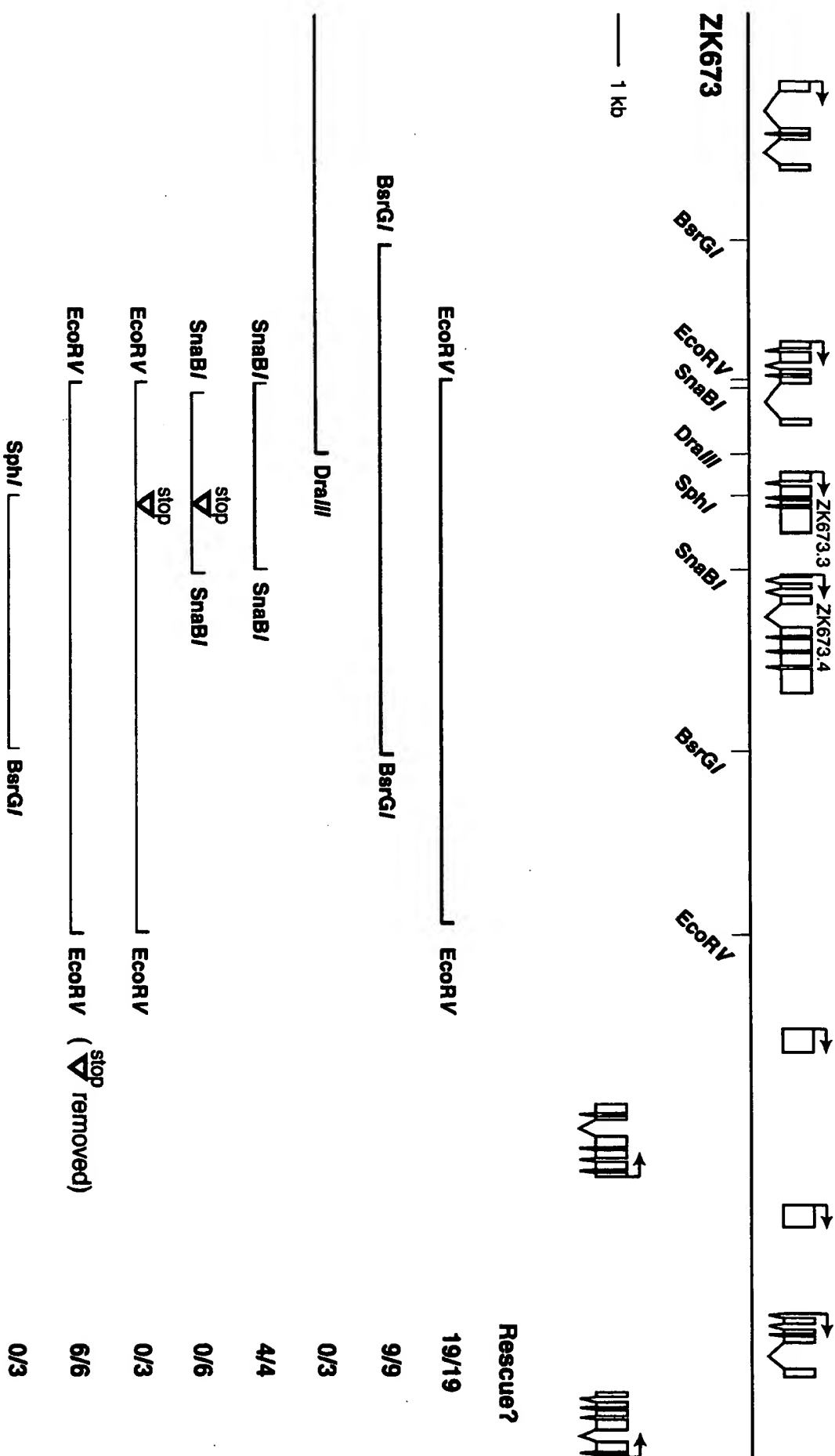




FIG. 6

LIN-56

MDHHAMRYRTAEFNKTTVRLLAEFIEKTGQNATIVNMDSFLEFFAYLNPTA 50  
PIPTVPEIEKQLLKSPi 100  
[REDACTED] HVIFEGLOIENTYCAHAKYSL 150  
ANRWCKVYTMIRSSLGEQFTKFDVRNFKSILQSFLDTFGEIDDDKDKDES 200  
SHFDECFEEMDSENVKIMESPQEEAAEKSKFSENLVEVKLEPIETHELD 250  
KTISDFSSSDIIDSQKLQNGCFPEKEVEQMDKYSNKLKDEASDKKYEKPG 300  
KKDYVEEEGYPAPIITDSEDEEA 322

69 R V GMETESDSAVTLSIDN S I T T IGYCRDPSPD VNQ K S RA TK FNSIF 128  
211 L EKALLMRESIAMTDNE VKV M A MSCHERMAT EKA H R RM YD VDFV 270  
176 I GNEVPCHRSIRVSDDDD A F T A LTDQKTIRQ KRD LS Y TV LR SLHY 235  
274 [REDACTED] LV NQQMEMTKVRSVNNNTD Y M IYVC MNDKYDMDK KELA MQRFKC VS LDEL 333  
\* \* \* \* \*

FIG. 7

|               |      |                       |                     |                |        |
|---------------|------|-----------------------|---------------------|----------------|--------|
|               |      | 10                    | 20                  | 30             | 40     |
|               |      | .....*                | .....*              | .....*         | .....* |
| consensus     | 1    | FDWEDYL---            | EETGARAAPVELF---    | DKQPVDSPNGFKV  | 34     |
| lin-61        | 146  | VNYVNNCi-d            | GEIVGQTSLSPKF---    | DEGKALLSKHRFKV | 181    |
| lin-61        | 23   | YLWESYLhqf            | EKGKTSFIPVEAF---    | NRNLTVPNFECVKE | 59     |
| lin-61        | 388  | FRWDEYL---            | EKESAETLPLDLF---    | KPMPSQERLDKFKV | 421    |
| hl(3)mbt      | 206  | WSWESYL---            | EEQKAITAPVSLFq---   | DSQAVTHNKNQFKL | 240    |
| hl(3)mbt      | 314  | FSWSQYM---            | CSTRAQAAPKHMf---    | VSQSHSPPLGFQV  | 347    |
| hl(3)mbt      | 422  | PCWEKYL---            | EETGASAVPTWAF-----  | KVRPPHSFLV     | 451    |
| tumor sup(Dm) | 819  | FRWSEYLk---           | SKGKDVAAPIHLf---    | LNPFPISPNCFEI  | 852    |
| tumor sup(Dm) | 926  | FSWSRYL---            | VKTGGKAAPRALFghl    | NMQQQMDVRNGFAV | 962    |
| tumor sup(Dm) | 1035 | FIWDDYI---            | SEVGGMAASKELF-----  | TPRQPMHEYQE    | 1064   |
| scmh1 (mouse) | 28   | FTWDKYL---            | KETCSVPAPVHCF-----  | KQSYTPPSNEFKI  | 60     |
| scml2 (human) | 139  | SSWPMFLl-k            | TLNGSEMASATLf-----  | KKEPPKPPLNNFKV | 174    |
|               |      | 50                    | 60                  | 70             | 80     |
|               |      | .....*                | .....*              | .....*         | .....* |
| consensus     | 35   | -----GMKLEAVDP-----   | RNPSLICVATVVEVKYR   | 61             |        |
| lin-61        | 182  | -----GQRLELLNY-----   | SNSTEIRVARIQEICGRR  | 208            |        |
| lin-61        | 60   | -----GVIFETVVHdydknc  | DSIQVRWFARIEKVCGYR  | 92             |        |
| lin-61        | 422  | iliskrvGLRLEAADM----- | CENQFICPATVKSVBHRL  | 455            |        |
| hl(3)mbt      | 241  | -----GMKLEGIDP-----   | QHPSMYFILTVAEVCGYR  | 267            |        |
| hl(3)mbt      | 348  | -----GMKLEAVDR-----   | MNPSLVCVASVTDVDSR   | 374            |        |
| hl(3)mbt      | 452  | -----NMKLEAVDR-----   | RNPALIRVASVEDVEDHR  | 478            |        |
| tumor sup(Dm) | 853  | -----GMKLEAIDP-----   | ENCSLFCVCVSIVEVRGYR | 879            |        |
| tumor sup(Dm) | 963  | -----GMHLEAEDL-----   | NDTGKICVATVTDILDER  | 989            |        |
| tumor sup(Dm) | 1065 | -----RMKLEVVDQ-----   | RNPCLIRPATVVTRKGYR  | 1091           |        |
| scmh1 (mouse) | 61   | -----SMKLEAQDP-----   | RNTTSTCIATVVGLTGAR  | 87             |        |
| scml2 (human) | 175  | -----GMKLEAIDK-----   | KNPYLICPATIGDVKGDE  | 201            |        |
|               |      | 90                    | 100                 | 110            | 120    |
|               |      | .....*                | .....*              | .....*         | .....* |
| consensus     | 62   | LLLHFD-----           | GWDDR-----          | YDFWCDADSPDIF  | 85     |
| lin-61        | 209  | MNVSITkdfpesl         | pdADDDRqvfesgSQY    | WIDEGSFFIF     | 246    |
| lin-61        | 93   | VLAQFI-----           | GAD-----            | TKFWNLISDDMP   | 114    |
| lin-61        | 456  | INVNFD-----           | GWDEE-----          | FDELYDVDSHDIL  | 479    |
| hl(3)mbt      | 268  | LRLHFD-----           | GYSEC-----          | HDFWVNANSPDIH  | 291    |
| hl(3)mbt      | 375  | FLVHFD-----           | NWDDT-----          | YDYWCDPSSPYIH  | 398    |
| hl(3)mbt      | 479  | IKIHFD-----           | GWSHG-----          | YDFWIDADHPDIH  | 502    |
| tumor sup(Dm) | 880  | LKLSFD-----           | GYSSM-----          | YDFWVNADSDQIF  | 903    |
| tumor sup(Dm) | 990  | IRVHFD-----           | GWDDC-----          | YDLWVHITSPYIH  | 1013   |
| tumor sup(Dm) | 1092 | VQLHLD-----           | CWPTE-----          | YYFWLEDDSPDLH  | 1115   |
| scmh1 (mouse) | 88   | LRLRLD-----           | GSDNK-----          | NDFWRLVDSSEIQ  | 111    |
| scml2 (human) | 202  | VHITFD-----           | GWSGA-----          | FDYWCKYDSRDIF  | 225    |
|               |      | 130                   |                     |                |        |
|               |      | .....*                | .....*              |                |        |
| consensus     | 86   | PVGWCEKNGHPLQPP       | 100                 |                |        |
| lin-61        | 249  | PVGFAAVNGYQLNAK       | 263                 |                |        |
| lin-61        | 115  | GLANAAM-SDPNMDK       | 128                 |                |        |
| lin-61        | 480  | PIGWCEAHSYVLQPP       | 494                 |                |        |
| hl(3)mbt      | 292  | PAGWFECTGHKLQLP       | 306                 |                |        |
| hl(3)mbt      | 399  | PVGWCQKQKPLTPP        | 413                 |                |        |
| hl(3)mbt      | 503  | PAGWCSKTGHPLQPP       | 517                 |                |        |
| tumor sup(Dm) | 904  | PPGWCDetarVLQAP       | 918                 |                |        |
| tumor sup(Dm) | 1014 | PCGWHEGRQQLIVPP       | 1028                |                |        |
| tumor sup(Dm) | 1116 | PIGWCEATSHELETP       | 1130                |                |        |
| scmh1 (mouse) | 112  | PIGNCEKNGGMLQPP       | 126                 |                |        |
| scml2 (human) | 226  | PAGWCRLTGDVLQPP       | 240                 |                |        |



[illegible]

|                                |  |                                 |           |                                 |                                     |                 |
|--------------------------------|--|---------------------------------|-----------|---------------------------------|-------------------------------------|-----------------|
| transformation of JIN-63 cDNA  | 21 P T E K G A F R P V Y N A F X M L D I Q | N - 7 C H E G V I P F E V V -   | - D Y D R | D Z I                           | V N S P A I N I S E V C G Y M A L A | E G A           |
| protein product of hsp 90A0315 | 12 V A - - - - -                           | S V P M T C L L I F K - - - - - | - - - - - | - V P I A O I V K E L G Y M A L | A L                                 | G F U           |
| protein product of Co 18C03.6  | 76 M Y D G M F Q F P V E A L               | O L L D N                       | K L H     | M N D P T A L E V V V           | P S L D P S I                       | K M F R W F G R |
|                                |  |                                 |           |                                 | T A V C G                           | T V A           |
|                                |  |                                 |           |                                 |                                     | F M C E L N     |
|                                |  |                                 |           |                                 |                                     | 15              |

[illegible]

translation of 115-61 cDNA 109  
Protein product of hsp 2450210 102  
Protein product of Co 16021.6 226

[illegible]

Translation of 11a-61 cDNA 306 K K V G Q R F E L I D P L Q G S L E A L I N F C R T C L I G A D G E A L S - - F P I N I N F H E P V G Y A E K - E L V  
 Protein product of hnp 3A5029 218 W F K E G K L E I D P L M - - L S C V A T I R K L A - G F L I G A D C E A A D G S D W F C Y H A Q P S F P V G Y A E I E I E L F 219  
 Protein product of Co Y460A.6 351 L K R V G Q K F E L I D P L D L K E C V A T I R K C K T P G F L I S P D E E I D D P S - F P I N I D H E F H A P V G Y A E K I E I K L D 4

| Translational of 11n-61 cDNA     | 378 | P P D - E P K C G F P P W   | Y L E R K S A E                               | P P L F P P S E N L D R F V I           | S K E V G L A L S A A D N G E | P I C P A T V K R V H G |
|----------------------------------|-----|---|---|---|-------------------------------|-------------------------|
| protein product of hsp 70A0019.5 | 281 | P P K C Y T N L P F K V I Y L E <th>S T O G I A P L T E R K D V P</th> <td>- - - H O F V G K L E A V D L</td> <td>- - - - - E E D L I C V A T V</td> <td>R N I H 35</td>  | S T O G I A P L T E R K D V P                 | - - - H O F V G K L E A V D L           | - - - - - E E D L I C V A T V | R N I H 35              |
| protein product of Ce 71001A.6   | 426 | R L A G C T E P G K F K V I Q Y L E <td>K O A E K P D L P P P S K E D N A H M F T G A</td> <td>L E A V G Q - - - - - E E Y W I P A T V</td> <td>N V H G 41</td> <td></td> | K O A E K P D L P P P S K E D N A H M F T G A | L E A V G Q - - - - - E E Y W I P A T V | N V H G 41                    |                         |

| Translation of 11S-61 cDNA     | 483 | R | L | N | 498 |
|--------------------------------|-----|---|---|---|-----|
| Protein product of bag 1A40915 | 386 | R | L | N | 410 |
| Protein product of Ce 148021.6 | 492 | R | L | N | 512 |

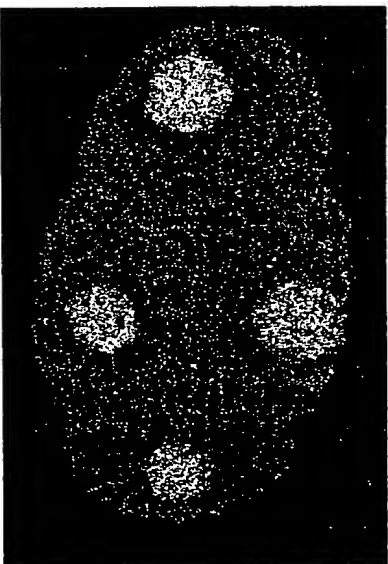
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WASHINGTON, D.C. 20540

FIG. 9A



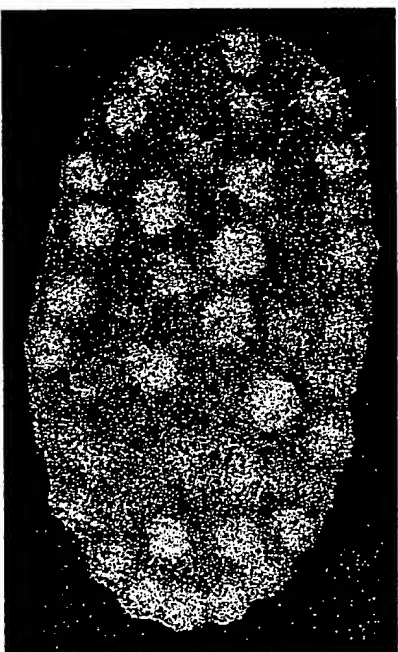
2-cell embryo

FIG. 9B



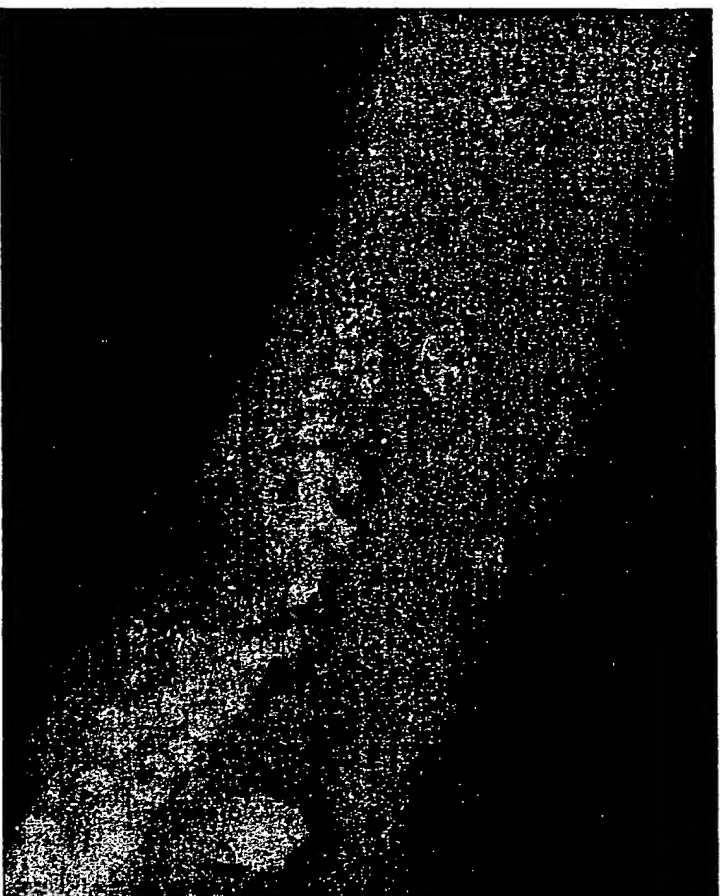
4-cell embryo

FIG. 9C



multicellular embryo

FIG. 9D



vulval region of an L4 larva



FIG. 10A

2-cell embryo

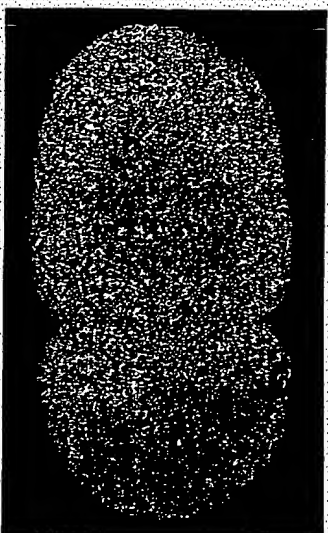


FIG. 10B

4-cell embryo

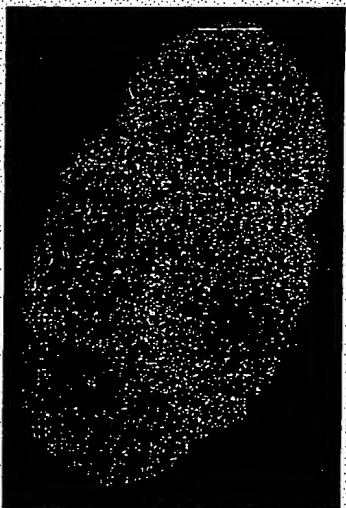
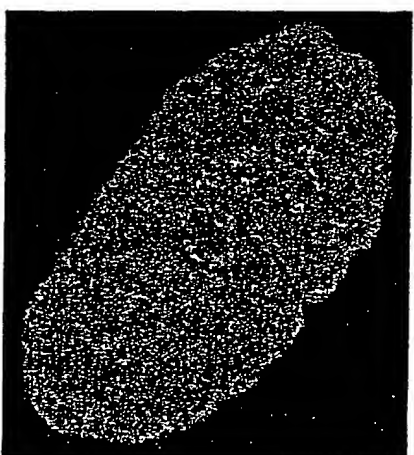


FIG. 10C

multicellular embryo



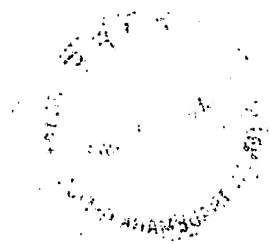
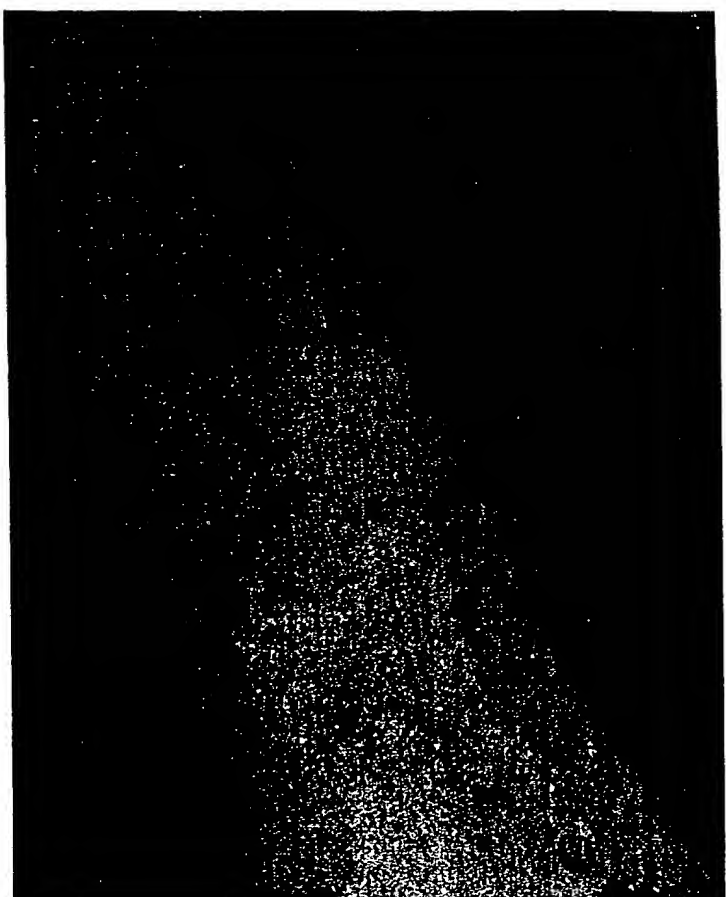


FIG. 10D



vulval region of an L4 larva



FIG. 11A

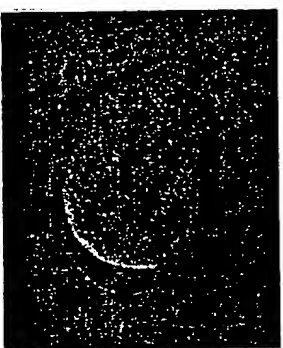


FIG. 11B

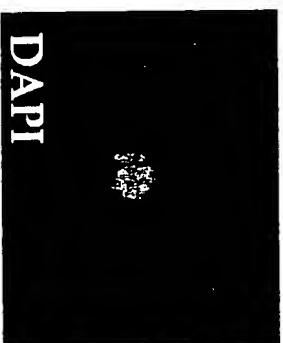


FIG. 11C

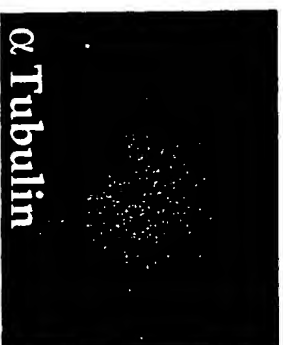




FIG. 12A



FIG. 12B



FIG. 12C



FIG. 12D



FIG. 12E



FIG. 12F



FIG. 12G



FIG. 12H





FIG. 13A

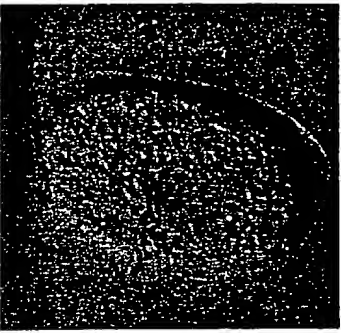


FIG. 13B



FIG. 13C

